

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 9, 2005, 20:59:41 ; Search time 39 seconds

(without alignments)
44.408 Million cell updates/sec

Title: US-10-706-265-2

Perfect score: 121
Sequence: 1 RRMCRKCYKGYCRKCR 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	87.6	18	2	polyphemus II -
2	103	85.1	18	2	polyphemus I - A
3	94	77.7	17	2	tachyplesin II pre
4	91	75.2	17	2	tachyplesin III -
5	88	72.7	17	2	tachyplesin I - ho
6	88	72.7	19	2	tachyplesin I prec
7	88	72.7	77	2	tachyplesin I prec
8	88	72.7	594	2	transport inhibito
9	51	42.1	64	2	toxin II-14 - scor
10	50	41.3	85	2	probable trypsin i
11	50	41.3	922	2	metalloproteinase
12	48.5	40.1	970	2	ORF MSV076 probabl
13	48	39.7	86	2	Na+-channel-blocki
14	48	39.7	90	2	probable trypsin i
15	48	39.7	1184	2	probable protein p
16	47	38.8	345	2	hypothetical prote
17	47	38.8	1620	2	hypothetical prote
18	46.5	38.4	83	2	p11 protein (clon
19	46.5	38.4	139	2	hypothetical prote
20	46.5	38.4	622	2	hypothetical prote
21	46	38.0	30	2	toxin II.6 - scor
22	46	38.0	376	2	hypothetical prote
23	46	38.0	650	2	endocycle-specific
24	46	38.0	749	2	mechanosensory pro
25	46	38.0	795	2	hypothetical prote
26	46	38.0	1390	2	insulin receptor -
27	45.5	37.6	143	2	neurotoxin I - sco
28	45	37.2	66	2	hypothetical prote
29	45	37.2	68	2	hypothetical prote

30	45	37.2	135	2	G84469	probable glycine-r
31	45	37.2	251	2	A55035	cysteine-rich prot
32	45	37.2	361	1	F64355	conserved hypothet
33	45	37.2	374	2	D81715	conserved hypothet
34	45	37.2	497	2	G81284	probable Ni/Fe-hyd
35	45	37.2	1148	2	A71446	hypothetical prote
36	44.5	36.8	144	2	T29558	hypothetical prote
37	44	36.4	131	2	T11557	cat protein - simi
38	44	36.4	132	2	T11564	hypothetical prote
39	44	36.4	392	2	T12311	hypothetical prote
40	44	36.4	598	2	T40676	latent transformin
41	44	36.4	1251	2	A57293	MEGF6 protein - ra
42	44	36.4	1574	2	T13954	hyperplastic discs
43	44	36.4	2895	2	T08437	similar to glibbere
44	43.5	36.0	108	2	G84522	hypothetical prote
45	43.5	36.0	217	2	T28343	hypothetical prote

ALIGNMENTS

RESULT 1

U0125
polyphemus II - Atlantic horseshoe crab
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: U0125
R:Miyaata, T.; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao, T.;
J. Biochem. 106, 663-668, 1989
A:Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin II,
A:Reference number: A91914; MUID:90110066; PMID:2514185
A:Accession: U0125
A:Molecule type: protein
A:Residues: 1-18 <MTX>
A:Cross-references: UNIPROT:P14216
C:Comment: The peptide is one of the antimicrobial peptides in the American horseshoe crab
F:4-17,8-13/Disulfide bonds: #status predicted
F:18/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 87.6%; Score 106; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.6e-07;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMCRKCYKGYCRKCR 18
DB 1 RRMCRKCYKGYCRKCR 18

RESULT 2

U0124
polyphemus I - Atlantic horseshoe crab
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: U0124
R:Miyaata, T.; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao, T.;
J. Biochem. 106, 663-668, 1989
A:Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin II,
A:Reference number: A91914; MUID:90110066; PMID:2514185
A:Accession: U0124
A:Molecule type: protein
A:Residues: 1-18 <MTX>
A:Cross-references: UNIPROT:P14215
C:Comment: The peptide is one of the antimicrobial peptides in the Atlantic horseshoe crab
F:4-17,8-13/Disulfide bonds: #status experimental
F:18/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 85.1%; Score 103; DB 2; Length 18;
Best Local Similarity 77.8%; Pred. No. 8.6e-07;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMCRKCYKGYCRKCR 18

||||:||||:||||:
Db 1 RMCRCVRCYRGICRYRKR 18

RESULT 3

B38345
Tachyplesin II precursor - horseshoe crab (Tachyplesus tridentatus)

C/Species: Tachyplesus tridentatus

C/Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 09-Jul-2004

C/Accession: B38345; J00123

R/Shigenaga, T.; Muta, T.; Toh, Y.; Tokunaga, F.; Iwanaga, S.

J. Biol. Chem. 265, 21350-21354, 1990

A/Title: Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localization

A/Reference number: A38345; MUID:91055956; PMID:2250028

A/Accession: B38345

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-77 <SH1>

A/Cross-references: UNIPROT:P14214; GB:J05689

R/Miyata, T.; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao, T.

J. Biochem. 106, 663-668, 1989

A/Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin II,

A/Reference number: A91914; MUID:90110066; PMID:2514185

A/Accession: J00123

A/Molecule type: protein

A/Residues: 24-40 <MT>

C/Comment: The peptide is one of the antimicrobial peptides found in the Japanese horses

F/26-39, 30-35/Disulfide bonds: #status predicted

F/40/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly

Query Match 77.7%; Score 94; DB 2; Length 77;
Best Local Similarity 76.5%; Pred. No. 3e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 4

JX0125
Tachyplesin III - horseshoe crab (Tachyplesus gigas)

C/Species: Tachyplesus gigas

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C/Accession: JX0125

R/Muta, T.; Fujimoto, T.; Nakajima, H.; Iwanaga, S.

J. Biochem. 106, 261-266, 1990

A/Title: Tachyplesins isolated from hemocytes of southeast Asian horseshoe crabs (Carcin

ssing intermediate of its precursor.

A/Reference number: JX0124; MUID:91035357; PMID:2229025

A/Accession: JX0125

A/Molecule type: protein

A/Residues: 1-17 <MT>

A/Cross-references: UNIPROT:P18252

A/Experimental source: hemocyte

C/Keywords: amidated carboxyl end

F/3-16, 7-12/Disulfide bonds: #status predicted

F/17/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 75.2%; Score 91; DB 2; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.6e-05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

2 RMCRCYRCYRGICRYRKR 18
:||:||||:||||:
Db 1 KMCRCVRCYRGICRYRKR 17

RESULT 5

A38824
Tachyplesin I - horseshoe crab (Tachyplesus gigas)

C/Species: Tachyplesus gigas

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C/Accession: A38824

R/Muta, T.; Fujimoto, T.; Nakajima, H.; Iwanaga, S.

J. Biochem. 106, 261-266, 1990

A/Title: Tachyplesins isolated from hemocytes of southeast Asian horseshoe crabs (Carcin

ssing intermediate of its precursor.

A/Reference number: JX0124; MUID:91035357; PMID:2229025

A/Accession: A38824

A/Molecule type: protein

A/Residues: 1-17 <MT>

A/Cross-references: UNIPROT:P23684

A/Experimental source: hemocyte

C/Keywords: amidated carboxyl end

F/3-16, 7-12/Disulfide bonds: #status predicted

F/17/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 72.7%; Score 88; DB 2; Length 17;
Best Local Similarity 64.7%; Pred. No. 6.2e-05;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

2 RMCRCYRCYRGICRYRKR 18
:||:||||:||||:
Db 1 KMCRCVRCYRGICRYRKR 17

RESULT 6

JX0124
Tachyplesin I precursor - horseshoe crab (Carcinoscorpius rotundicauda)

C/Species: Carcinoscorpius rotundicauda

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C/Accession: JX0124

R/Muta, T.; Fujimoto, T.; Nakajima, H.; Iwanaga, S.

J. Biochem. 106, 261-266, 1990

A/Title: Tachyplesins isolated from hemocytes of southeast Asian horseshoe crabs (Carcin

ssing intermediate of its precursor.

A/Reference number: JX0124; MUID:91035357; PMID:2229025

A/Accession: JX0124

A/Molecule type: protein

A/Residues: 1-19 <MT>

A/Cross-references: UNIPROT:P23684

A/Experimental source: hemocyte

C/Keywords: amidated carboxyl end

F/1-17/Product: tachyplesin I #status experimental <MT>

F/3-16, 7-12/Disulfide bonds: #status predicted

F/17/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly

Query Match 72.7%; Score 88; DB 2; Length 19;
Best Local Similarity 64.7%; Pred. No. 6.6e-05;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

2 RMCRCYRCYRGICRYRKR 18
:||:||||:||||:
Db 1 KMCRCVRCYRGICRYRKR 17

RESULT 7

A38345
Tachyplesin I precursor - horseshoe crab (Tachyplesus tridentatus)

C/Species: Tachyplesus tridentatus

C/Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 09-Jul-2004

C/Accession: A38345; A30068

R/Shigenaga, T.; Muta, T.; Toh, Y.; Tokunaga, F.; Iwanaga, S.

J. Biol. Chem. 265, 21350-21354, 1990

A/Title: Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localization

A/Reference number: A38345; MUID:91055956; PMID:2250028

A/Accession: A38345

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-77 <SH1>

A/Cross-references: UNIPROT:P14213; GB:M57242; GB:J05689; NID:G161659; PID:G161660

R/Nakamura, T.; Furunaka, H.; Miyata, T.; Tokunaga, F.; Muta, T.; Iwanaga, S.; Niwa, M.

J. Biol. Chem. 263, 16709-16713, 1988

A/Title: Tachyplesin, a class of antimicrobial peptide from the hemocytes of the horseshoe

A:Reference number: A30068; MUID:89034158; PMID:3141410
A:Accession: A30068
A:Molecule type: protein
A:Residues: 24-40 <NAK>

Query Match 72.7%; Score 88; DB 2; Length 77;
Best Local Similarity 64.7%; Pred. No. 0.00017;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 RWCYKCYKGYCYRKR 18
DB 24 KWCFCYCYRGICYRRCR 40

RESULT 8

Transport inhibitor response protein TIR1 [imported] - Arabidopsis thaliana
N:Alternate names: protein T20010.80
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48087; T51946

R:Obermaier, B.; Ottenweilder, B.; Duchemin, D.; Zeitler, K.; Mewes, H.W.; Rudd, S.; Len
submitted to the EMBL Data Library, May 1997

A:Reference number: 224484
A:Accession: T48087

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-594 <OBE>

A:Cross-references: UNIPROT:O24660; EMBL:AL163816

A:Experimental source: cultivar Columbia; BAC clone T20010

R:Ruegger, M.; Dewey, E.; Gray, B.; Hobbie, L.; Turner, J.; Estelle, M.
submitted to the EMBL Data Library, May 1997

A:Description: The TIR1 protein of Arabidopsis functions in auxin response and is related
A:Reference number: 225881
A:Accession: T51946

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-594 <RUE>

A:Cross-references: EMBL:AF005047; PIDN:AAB69175.1

C:Genetics:
A:Gene: TIR1
A:Map position: 3
A:Intons: 156/2; 320/3
A>Note: T20010.80

Query Match 43.0%; Score 52; DB 2; Length 594;
Best Local Similarity 61.5%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 RWCYKCYKGYCY 14
DB 42 RWCRRKRVIGNCY 54

RESULT 9

S32789
toxin II-14 - scorpion (Centruroides noxius)

C:Species: Centruroides noxius
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S32789

R:Posasani, L.D.; Martin, B.M.; Svendsen, I.; Rode, G.S.; Erickson, B.W.
Biochem. J. 229, 739-750, 1985

A:Title: Scorpion toxin from Centruroides noxius and Tityus serrulatus. Primary structure
A:Reference number: S32789; MUID:86025386; PMID:4052021

A:Accession: S32789

A:Status: preliminary
A:Molecule type: protein

A:Residues: 1-64 <POS>

A:Cross-references: UNIPROT:P15223
C:Superfamily: scorpion neurotoxin

Query Match 42.1%; Score 51; DB 2; Length 64;
Best Local Similarity 47.4%; Pred. No. 6.3;

Matches 9; Conservative 2; Mismatches 4; Indels 4; Gaps 1;
QY 4 CYRKYK----GYCYRKR 18
DB 11 CKKNCYKLGKNDYCNRCR 29

RESULT 10

Probable trypsin inhibitor [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: C84867

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffett, K.S.; Cronin, L.A.; Shen, M.; Vanacker, S.E.; Unayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: C84867

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-85 <STO>

A:Cross-references: UNIPROT:O22867; GB:AE02093; NID:92289007; PIDN:AAB64336.1; GSPDB:GNC

C:Genetics:
A:Gene: At2g43530
A:Map position: 2

Query Match 41.3%; Score 50; DB 2; Length 85;
Best Local Similarity 43.8%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 WCYKCYKGYCYRKR 18
DB 45 YCMARVPSLCYRNCR 60

RESULT 11

T37256
metalloproteinase sup-17 - Caenorhabditis elegans

N:Alternate names: ADAM 10 protein
C:Species: Caenorhabditis elegans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37256; T20395

R:Men, C.; Wechslein, M.M.; Greenwald, I.
Development 124, 4759-4767, 1997

A:Title: SUP-17, a Caenorhabditis elegans ADAM protein related to Drosophila KUZBANIAN, 2
A:Reference number: 221649; MUID:98088688; PMID:9428412

A:Accession: T37256

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-922 <MEN>

A:Cross-references: UNIPROT:O46354; EMBL:AF024614; NID:92739036; PIDN:AAB97161.1; PID:927

R:Lenhard, N.
submitted to the EMBL Data Library, June 1997

A:Reference number: 219266

A:Accession: T20395

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-922 <WIL>

A:Cross-references: EMBL:Z96047; PIDN:CAB09416.1; GSPDB:GN00019; CESP:sup-17

A:Experimental source: clone D13
A:Gene: sup-17
A:Map position: 1

Query Match 41.3%; Score 50; DB 2; Length 92;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 9; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

Db 703 YKGYCIDIFRRCR 714

RESULT 12

T28234
ORF MSV076 probable spheroidin - Melanoplus sanguinipes entomopoxvirus
C/Species: Melanoplus sanguinipes entomopoxvirus
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C/Accession: T28234
R/Accession: T28234
R/Accession: T28234
J. Virol. 73, 533-552, 1999
A/Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A/Reference number: Z20484; MUID:99102612; PMID:9847359
A/Accession: T28234
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-970 <AFO>
A/Cross-references: UNIPROT:Q9Y1W19; EMBL:AF063866; NID:g4049647; PIDN:AAC97813.1; PID:g4
C/Genetics:
A/Note: MSV076

Query Match 40.1%; Score 48.5; DB 2; Length 970;
Best Local Similarity 52.9%; Pred. No. 79;
Matches 9; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

OY 3 WCYRKYCYG-YCYRKR 18
Db 847 WPNRCKRGCVVPCR 863

RESULT 13

JN0671
Na+-channel-blocking toxin (clone cngtIV) precursor - scorpion (Centruroides noxius)
C/Species: Centruroides noxius
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C/Accession: JN0671
R/Accession: JN0671
R/Accession: JN0671
J. Biol. Chem. 269, 165-171, 1994
A/Title: Cloning and characterization of cDNAs that code for Na+-channel-blocking toxins
A/Reference number: JN0669; MUID:93292983; PMID:8390386
A/Accession: JN0671
A/Molecule type: mRNA
A/Residues: 1-86 <BEC>
A/Cross-references: UNIPROT:P45665; GB:L05062; NID:g304570; PIDN:AAA28287.1; PID:g304571
A/Experimental source: venom gland
C/Superfamily: scorpion neurotoxin
C/Keywords: toxin
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-86/Product: Na+-channel-blocking toxin (clone cngtIV) #status predicted <MAT>

Query Match 39.7%; Score 48; DB 2; Length 86;
Best Local Similarity 42.1%; Pred. No. 18;
Matches 8; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

OY 4 CYRKYC---GYCRKR 18
Db 30 CKKNCYKLGENDYCNRECK 48

RESULT 14

B84867
probable trypsin inhibitor [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: B84867
R/Accession: B84867
R/Accession: B84867
J. Biol. Chem. 274, 10545-10552, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: B84867
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-90 <STO>
A/Cross-references: UNIPROT:O22866; GB:AE002093; NID:g2288995; PIDN:AAB64324.1; GSPDB:GN
C/Genetics:
A/Gene: At2g43520
A/Map position: 2

Query Match 39.7%; Score 48; DB 2; Length 90;
Best Local Similarity 37.5%; Pred. No. 19;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 3 WCYRKYCYG-CYRKR 18
Db 44 YCAPRIFFSPCYNCR 59

RESULT 15

D86387
probable protein P-type transporting ATPase [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: D86387
R/Accession: D86387
R/Accession: D86387
J. Biol. Chem. 274, 10545-10552, 1999
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: D86387
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1184 <STO>
A/Cross-references: UNIPROT:P57792; GB:AE005172; NID:g11079517; PIDN:AA929228.1; GSPDB:GN
C/Genetics:
A/Map position: 1

Query Match 39.7%; Score 48; DB 2; Length 1184;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 WCYRKYCYG-CY 14
Db 915 WCYRKYCYG-CY 926

Search completed: May 9, 2005, 21:15:12
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: May 9, 2005, 20:56:23 ; Search time 170 Seconds
(without alignments)
54.220 Million cell updates/sec

Title: US-10-706-265-2

Perfect score: 121
Sequence: 1 RRMCRKCYKGYCKR 18

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	87.6	18	1 PPM2 LIMPO	P14216 limulus pol
2	103	85.1	18	1 PPM2 LIMPO	P14215 limulus pol
3	94	77.7	17	1 TAC2 TACR	P14214 tachyples
4	91	75.2	17	1 TAC3 TACGI	P18252 tachyples
5	88	72.7	17	1 TAC1 TACGI	P14213 tachyples
6	88	72.7	17	1 TAC1 TACR	P14213 tachyples
7	54	44.6	398	2 OBNAX2	OBNAX2 homo sapien
8	52	43.0	143	2 O6CHR2	O6chr2 yarrowia li
9	52	43.0	594	2 O24660	O24660 arabidopsis
10	52	43.0	1040	2 Q7RGR2	Q7RGR2 plasmodium
11	51	42.1	64	2 O6V422	O6V422 centruroid
12	51	42.1	86	2 SCX1 CENNO	P15223 centruroid
13	50	41.3	83	2 O6Z2P9	O6z2p9 arabidopsis
14	50	41.3	83	2 O6Z2Z9	O6z2z9 arabidopsis
15	50	41.3	83	2 O6Z2Z9	O6z2z9 arabidopsis
16	50	41.3	83	2 O6Z2R4	O6z2r4 arabidopsis
17	50	41.3	83	2 O6Z2R9	O6z2r9 arabidopsis
18	50	41.3	85	1 IT15 ARATH	O22867 arabidopsis
19	50	41.3	85	2 O6Z2T8	O6z2t8 arabidopsis
20	50	41.3	397	2 O6AY88	O6ay88 rattus norv
21	50	41.3	922	2 O6A354	O6a354 caenorhabdi
22	50	41.3	2040	2 O6ORQ1	O6orq1 brachydantio
23	49	40.5	448	2 O6CED2	O6ced2 yarrowia li
24	49	40.5	787	2 O8TC27	O8tc27 homo sapien
25	49	40.5	787	2 O8TC42	O8tc42 homo sapien
26	48.5	40.1	970	2 O9YMA9	O9yma9 melanoplus
27	48.5	40.1	973	2 O6SS55	O6ss55 calliptamus
28	48	39.7	64	2 O6V4Z3	O6v4z3 centruroid
29	48	39.7	68	1 SCX6 CENIL	P60163 centruroid
30	48	39.7	85	1 SCX6 CENIL	P721K5 centruroid
31	48	39.7	86	1 SCXY_CENNO	P45665 centruroid

32	48	39.7	90	1 IT14 ARATH	O22866 arabidopsis
33	48	39.7	90	2 O6Z2L0	O6z2l0 arabidopsis
34	48	39.7	90	2 O6Z2T9	O6z2t9 arabidopsis
35	48	39.7	406	2 O9W404	O9w404 drosophila
36	48	39.7	415	2 O8IKR6	O8ikr6 plasmodium
37	48	39.7	708	2 O9LGM8	O9lgm8 oryza sativ
38	48	39.7	1184	1 ALAC ARATH	P57792 arabidopsis
39	47.5	39.3	199	2 O9D9Z9	O9d9z9 m musc muscu
40	47	38.8	107	2 O9S0I9	O9s0i9 caenorhabdi
41	47	38.8	111	2 O9GM17	O9gm17 macaca fasc
42	47	38.8	111	2 O6MR53	O6mr53 ddelioidi
43	47	38.8	563	2 O7SZX6	O7szx6 brachydantio
44	47	38.8	563	2 O7SZX6	O7szx6 brachydantio
45	47	38.8	570	2 O6PGZ4	O6pgz4 brachydantio

ALIGNMENTS

```
RESULT 1
PPM2 LIMPO
ID PPM2 LIMPO STANDARD, PRT, 18 AA.
AC P14216;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Polypheumus II.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_TaxID=6850;
RN [1]
RP SEQUENCE.
RX MEDLINE=90110066; PubMed=2514185;
RA Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M.,
RA Takao T., Shimomishi Y.;
RT "Antimicrobial peptides, isolated from horseshoe crab hemocytes,
RT tachyplesin II and polypheumins I and II: chemical structures and
RT biological activity".
RL J. Biochem. 106:663-668(1989).
CC -1- FUNCTION: Significantly inhibits the growth of Gram-negative and
CC Gram-positive bacteria.
CC -1- TISSUE SPECIFICITY: Hemocytes.
CC -1- SIMILARITY: Belongs to the tachyplesin/polypheumins family.
DR PIR: J00125; J00125.
DR HSSP; P14213; IM42.
KW Amidation; Antibiotic; Direct protein sequencing.
FT DISULFID 4 17 By similarity.
FT DISULFID 8 13 By similarity.
FT MOD RES 18 18 Arginine amide.
SQ SEQUENCE 18 AA; 2431 MW; E402A109D2923504 CRC64;

Query Match 87.6%; Score 106; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.9e-07;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRMCRKCYKGYCKR 18
DB 1 RRMCRKCYKGYCKR 18
|||||:|||||
1 RRMCRKCYKGYCKR 18
1 RRMCRKCYKGYCKR 18

RESULT 2
PPM2 LIMPO
ID PPM2 LIMPO STANDARD, PRT, 18 AA.
AC P14215;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Polypheumus I.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_TaxID=6850;
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RN [1]
RP SEQUENCE AND DISULFIDE BONDS.
RX MEDLINE=90110066; PubMed=2514185;
RA Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M.,
RA Takao T., Shimomishi Y.;
RT "Antimicrobial peptides, isolated from horseshoe crab hemocytes,
RT tachyplesin II, and polyphemusins I and II: chemical structures and
RT biological activity.";
RL J. Biochem. 106:663-668(1989).
CC -1- FUNCTION: Significantly inhibits the growth of Gram-negative and
CC Gram-positive bacteria.
CC -1- TISSUE SPECIFICITY: Hemocytes.
CC -1- SIMILARITY: Belongs to the tachyplesin/polyphemusin family.
DR PIR: J00124; J00124.
KM HSP; P14213; IMA2.
FT DISULFID 4 17
FT DISULFID 8 13
FT MOD RES 18 18 Arginine amide.
SQ SEQUENCE 18 AA; 2459 MW; FB3FA109D2923504 CRC64;

Query Match 85.1%; Score 103; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 1.2e-06;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RMCYRKYCYRKYRKR 18
DB 1 RMCYRKYCYRKYRKR 18

RESULT 3
TAC2_TAC2R STANDARD; PRT; 77 AA.
ID TAC2_TAC2R
AC P14214;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tachyplesin II precursor.
OS Tachyplesin tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachyplesus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N. A.
RX MEDLINE=91065956; PubMed=2250028;
RA Shigenaga T., Mura T., Toh Y., Tokunaga F., Iwanaga S.;
RT "Antimicrobial tachyplesin peptide precursor. cDNA cloning and
RT cellular localization in the horseshoe crab (Tachyplesus
RT tridentatus).";
RL J. Biol. Chem. 265:21350-21354(1990).
RN [2]
RP SEQUENCE OF 24-40.
RX MEDLINE=90110066; PubMed=2514185;
RA Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M.,
RA Takao T., Shimomishi Y.;
RT "Antimicrobial peptides, isolated from horseshoe crab hemocytes,
RT tachyplesin II, and polyphemusins I and II: chemical structures and
RT biological activity.";
RL J. Biochem. 106:663-668(1989).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=94110249; PubMed=8282718;
RA Shigenaga T., Takayenoki Y., Kawasaki S., Seki N., Mura T., Toh Y.,
RA Ito A., Iwanaga S.;
RT "Separation of large and small granules from horseshoe crab
RT (Tachyplesus tridentatus) hemocytes and characterization of their
RT components.";
RL J. Biochem. 114:307-316(1993).
CC -1- FUNCTION: Significantly inhibits the growth of Gram-negative and
CC Gram-positive bacteria.
CC -1- SUBCELLULAR LOCATION: S-granules.
CC -1- TISSUE SPECIFICITY: Hemocytes.
CC -1- SIMILARITY: Belongs to the tachyplesin/polyphemusin family.

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DR PIR: B38345; B38345.
DR HSP; P14213; IMA2.
KM Amidation; Antibiotic; Cleavage on pair of basic residues;
KW Direct protein sequencing; Signal.
FT SIGNAL 1 23
FT PEPTIDE 24 40 Tachyplesin II.
FT PROPEP 41 77 By similarity.
FT DISULFID 26 39 By similarity.
FT DISULFID 30 35 By similarity.
FT MOD_RES 40 40 Arginine amide (G-41 provides amide
FT group).
FT DOMAIN 69 77 Asp/Glu-rich (acidic).
SQ SEQUENCE 77 AA; 9335 MW; 6EBE57A4A652AEFF CRC64;

Query Match 77.7%; Score 94; DB 1; Length 77;
Best Local Similarity 76.5%; Pred. No. 6e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RMCYRKYCYRKYRKR 18
DB 24 RMCYRKYCYRKYRKR 40

RESULT 4
TAC3_TAC3I STANDARD; PRT; 17 AA.
ID TAC3_TAC3I
AC P18252;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tachyplesin III.
OS Tachyplesus gigas (Southeast Asian horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachyplesus.
OX NCBI_TaxID=6852;
RN [1]
RP SEQUENCE.
RX MEDLINE=91035357; PubMed=2229025;
RA Mura T., Fujimoto T., Nakajima H., Iwanaga S.;
RT "Tachyplesin isolated from hemocytes of Southeast Asian horseshoe
RT crabs (Carcinoseorpius rotundicauda and Tachyplesus gigas):
RT identification of a new tachyplesin, tachyplesin III, and a processing
RT intermediate of its precursor.";
RL J. Biochem. 108:261-266(1990).
CC -1- FUNCTION: Significantly inhibits the growth of Gram-negative and
CC Gram-positive bacteria.
CC -1- TISSUE SPECIFICITY: Hemocytes.
CC -1- SIMILARITY: Belongs to the tachyplesin/polyphemusin family.
DR PIR: JX0125; JX0125.
DR HSP; P14213; IMA2.
KM Amidation; Antibiotic; Direct protein sequencing.
FT DISULFID 3 16 By similarity.
FT DISULFID 7 12 Arginine amide.
FT MOD_RES 17 17 Arginine amide.
SQ SEQUENCE 17 AA; 2241 MW; E9E08CE9D2923C94 CRC64;

Query Match 75.2%; Score 91; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 3.9e-05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 RMCYRKYCYRKYRKR 18
DB 1 RMCYRKYCYRKYRKR 17

RESULT 5
TAC1_TAC1I STANDARD; PRT; 17 AA.
ID TAC1_TAC1I
AC P23684;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tachyplesin I.

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OS Tachyplesus gigas (Southeast Asian horseshoe crab), and
 OS Carcinoscropsus rotundicauda (Southeast Asian horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Tachyplesus.
 RX NCBI_TaxID=6852, 6848;
 RN (1)
 RP SEQUENCE.
 RC SPECIES=C. rotundicauda, and T. gigas;
 RX MEDLINE=91035357; PubMed=2229025;
 RA Muta T., Fujimoto T., Nakajima H., Iwanaga S.;
 RT "Tachyplesin isolated from hemocytes of Southeast Asian horseshoe
 RT crabs (Carcinoscropsus rotundicauda and Tachyplesus gigas):
 RT identification of a new tachyplesin, tachyplesin III, and a processing
 RT intermediate of its precursor.";
 RL J. Biochem. 108:261-266(1990).
 CC -1- SIMILARITY: Belongs to the tachyplesin/polymyxin family.
 DR PIR: A38824; A38824.
 DR PIR: JX0124; JX0124.
 DR HSSP: P14213; IMA2.
 KW Amidation; Antibiotic; Direct protein sequencing.
 FT DISULFID 3 16
 FT DISULFID 7 12
 FT MOD_RES 17 17 Arginine amide.
 SQ SEQUENCE 17 AA; 2269 MW; E9E09BD9D2923C94 CRC64;
 Query March 72.7%; Score 88; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 9.4e-05;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 RWCYRKCYGKYCYRRCR 18
 Db 1 KMCFRVCTRGICYRRCR 17
 RESULT 6
 TACT TACTR STANDARD; PRT; 77 AA.
 AC P14213;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Tachyplesin I precursor.
 OS Tachyplesus tridentatus (Japanese horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Tachyplesus.
 RX NCBI_TaxID=6853;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91065956; PubMed=2250028;
 RA Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.;
 RT "Antimicrobial tachyplesin peptide precursor. cDNA cloning and
 RT cellular localization in the horseshoe crab (Tachyplesus
 RT tridentatus).";
 RL J. Biol. Chem. 265:21350-21354(1990).
 RN (2)
 RP SEQUENCE OF 24-40, AND DISULFIDE BONDS.
 RX MEDLINE=89034158; PubMed=3141410;
 RA Nakamura T., Furunaka H., Miyata T., Tokunaga F., Muta T., Iwanaga S.,
 RA Niwa M., Takao T., Shimomishi Y.;
 RT "Tachyplesin, a class of antimicrobial peptide from the hemocytes of
 RT the horseshoe crab (Tachyplesus tridentatus). Isolation and chemical
 RT structure.";
 RL J. Biol. Chem. 263:16709-16713(1988).
 RN (3)
 RP STRUCTURE BY NMR OF 24-40.
 RX MEDLINE=90368729; PubMed=2394727;
 RA Kawano K., Yoneya T., Miyata T., Yoshikawa K., Tokunaga F., Terada Y.,
 RA Iwanaga S.;
 RT "Antimicrobial peptide, tachyplesin I, isolated from hemocytes of the
 RT horseshoe crab (Tachyplesus tridentatus). NMR determination of the
 RT beta-sheet structure.";
 RL J. Biol. Chem. 265:15365-15367(1990).
 RN (4)

RP STRUCTURE BY NMR OF 24-40.
 RX MEDLINE=93257488; PubMed=8490053; DOI=10.1016/0167-4838(93)90183-R;
 RA Tamamura H., Kuroda M., Masuda M., Otake A., Funakoshi S.,
 RA Nakashima H., Yamamoto N., Maki M., Matsumoto A., Lancelin J.-M.,
 RA Konda D., Tate S., Inagaki F., Fujii N.;
 RT "A comparative study of the solution structures of tachyplesin I and a
 RT novel anti-HIV synthetic peptide, T22 (Tyr5,12, Lys7)-polymyxin
 RT II), determined by nuclear magnetic resonance.";
 RL Biochim. Biophys. Acta 1163:209-216(1993).
 RN (5)
 RP CHARACTERIZATION.
 RX MEDLINE=94110249; PubMed=8282718;
 RA Shigenaga T., Takayenoki Y., Kawasaki S., Seki N., Muta T., Toh Y.,
 RA Ito A., Iwanaga S.;
 RT "Separation of large and small granules from horseshoe crab
 RT (Tachyplesus tridentatus) hemocytes and characterization of their
 RT components.";
 RL J. Biochem. 114:307-316(1993).
 CC -1- FUNCTION: Significantly inhibits the growth of Gram-negative and
 CC Gram-positive bacteria.
 CC -1- SUBCELLULAR LOCATION: S-granules.
 CC -1- TISSUE SPECIFICITY: Hemocytes.
 CC -1- SIMILARITY: Belongs to the tachyplesin/polymyxin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 DR EMBL: M57242; AAA63538.1; -
 DR PIR: A38345; A38345.
 DR PDB: IMA2; NMR; A=24-40.
 DR PDB: IMA4; NMR; A=24-40.
 DR PDB: IMA5; NMR; A=24-40.
 DR PDB: IMA6; NMR; A=24-40.
 KW 3D-structure; Amidation; Antibiotic; Direct protein sequencing; Signal.
 KW Cleavage on pair of basic residues;
 FT SIGNAL 1 23 Tachyplesin I.
 FT PEPTIDE 24 40
 FT PROPEP 41 77
 FT DISULFID 26 39
 FT DISULFID 30 35
 FT MOD_RES 40 40 Arginine amide (G-41 provides amide group).
 FT DOMAIN 69 77 Asp/Glu-rich (acidic).
 SQ SEQUENCE 77 AA; 9349 MW; B940CAA4A641335F CRC64;
 Query March 72.7%; Score 88; DB 1; Length 77;
 Best Local Similarity 64.7%; Pred. No. 0.00035;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 RWCYRKCYGKYCYRRCR 18
 Db 24 KMCFRVCTRGICYRRCR 40
 RESULT 7
 OBNAX2 PRELIMINARY; PRT; 398 AA.
 AC OBNAX2;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Hypothetical protein FLJ34633.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.

RC TISSUE:Kidney;
 RX PubMed:14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Odayashi M., Nishi T., Shibahara T., Tanaka K., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosotani T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa M., Omura Y.,
 RA Abe K., Kamihara K., Katsura N., Sato K., Tanikawa M., Yamazaki M.,
 RA Niimiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirao K., Chida Y., Ishida S.,
 RA Oono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Yoshino K., Yuuki H., Oshima A., Sasaki N., Aotuka S.,
 RA Yushikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Oono T., Yamada K., Fujii Y., Ozaki K., Hirao K., Omori Y., Okamoto S.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsunuma K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mitsuhashi Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs";
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL; AK01952; BAC03775.1; --
 SQ SEQUENCE 398 AA; 43613 MW; BF1BD537D322A8D2 CRC64;

Query Match 44.6%; Score 54; DB 2; Length 398;
 Best Local Similarity 38.9%; Pred. No. 33;
 Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 RRCYRCYKCYKCR 18
 DB 79 RPYWMCRAFCRCR 96

RESULT 8
 O6CHR2 PRELIMINARY; PRT; 143 AA.
 AC O6CHR2;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Similarity (Fragment).
 GN ORFNames=YAL10A06039g;
 OS Yarrowia lipolytica CLIB99.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 CX NCBI_TaxID=284591;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RG Genolevures;
 RA Lafontaine I., de Montigny J., Marcq C., Neveglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anhouart V., Babet V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Desjardes A., Boyer J., Catolico L., Confanier F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerret A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicand J.M., Nikolski M., Oztas S., Ozer-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,

RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382127; CAG83724.1; --
 FT NON TER 1
 SQ SEQUENCE 143 AA; 16431 MW; 4CE3C9A00F66398E CRC64;

Query Match 43.0%; Score 52; DB 2; Length 143;
 Best Local Similarity 53.8%; Pred. No. 25;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 RRCYRCYKCYC 13
 DB 65 RRCCKMCSREYC 77

RESULT 9
 O24660 PRELIMINARY; PRT; 594 AA.
 AC O24660;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)
 DE Transport inhibitor response 1 (TIR1) (Putative transport inhibitor
 DE response TIR1, AtFBL1 protein).
 GN Name=TIR1; Synonyms=At3G62980, T20010.80;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eustosids.IT; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ruegger M., Dewey E., Gray B., Hobbie L., Turner J., Estelle M.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Obermaier B., Oetemaelder B., Duchemin D., Zeitler K., Mewes H.W.,
 RA Rüdelt S., Lemke K., Mayer K.F.X., Quetier F., Salanoubat M.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C.C., Toriumi M., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Chen H., Chen R., Jones T., Kim C.J., Nguyen M.,
 RA Palm C.J., Shim P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
 RA Ecker J.R., Theologis A.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF05048; AAB69176.1; --
 DR EMBL; AF163816; CAB87743.1; --
 DR EMBL; AF005047; AAB69175.1; --
 DR EMBL; BT001946; AAN71945.1; --
 DR PIR; T48087; T48087.
 DR InterAct; O24660; --
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007089; LRR_cys.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00560; LRR_1; 2.
 DR SMART; SM00256; FBOX; 1.
 SQ SEQUENCE 594 AA; 66798 MW; 9E19D5DABF40D07 CRC64;

Query Match 43.0%; Score 52; DB 2; Length 594;
Best Local Similarity 61.5%; Pred. No. 85;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 RWCYKCYKCYC 14
DB 42 RWCRRKVFIGNCY 54

RESULT 10
Q7RGR2 PRELIMINARY; PRT; 1040 AA.
Q7RGR2;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE WD-repeat protein p103.
DE Name=PY04284;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
RX PubMed=1236865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiolini S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalom J.J., van Aken S.B., Riedmiller S.B., Feldlyum T.V.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- SIMILARITY: Contains 8 WD repeats.
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL: AAB01001288; EAA16119.1.
DR InterPro: IPR001045; NAO reductase_N.
DR InterPro: IPR001580; WD40.
DR InterPro: IPR011046; WD40-like.
DR Pfam: PF00400; WD40; 8.
DR ProDom: PD000018; WD40; 1.
DR PROSITE: PS00082; WD_REPEATS_2; 2.
DR PROSITE: PS02994; WD_REPEATS_REGION; 3.
DR Repeat: WD repeat.
KW SEQUENCE 1040 AA; 119229 MW; FA6581547817C46C CRC64;

Query Match 43.0%; Score 52; DB 2; Length 1040;
Best Local Similarity 61.5%; Pred. No. 14e02;
Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 RWCYKCYKCYC 13
DB 277 RWCYKCYKCYC 287

RESULT 11
Q6V4Z2 PRELIMINARY; PRT; 64 AA.
Q6V4Z2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Beta-toxin (Fragment).
OS Centruroides noxius (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butidae; Butioidae; Butidae; Centruroides.

OX NCBI_TaxID=6878;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhu S.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (by similarity).
CC -1- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
DR EMBL: AY351298; AAR08033.1; -.
DR HSSP: P01491; 1B3C.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO: GO:0005515; F:protein binding; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR003614; Knt1.
DR InterPro: IPR001219; Neurotoxin.
DR InterPro: IPR002061; Scorpion_toxinL.
DR Pfam: PF00537; Toxin_3; 1.
DR PRINTS: PR00285; SCORPNTOXIN.
DR ProDom: PD000908; Scorpion_toxinL; 1.
DR SMART: SM00505; Knt1; 1.
FT NON_TER 1
FT NON_TER 64
SQ SEQUENCE 64 AA; 7248 MW; 082F5D95E2A289FD CRC64;

Query Match 42.1%; Score 51; DB 2; Length 64;
Best Local Similarity 47.4%; Pred. No. 16;
Matches 9; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QY 4 CYRKCYK---GYCKR 18
DB 11 CKKCYKKGKNDYCNRECR 29

RESULT 12
SCX1_CENNO STANDARD; PRT; 86 AA.
AC P15223; Q26460; (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-DEC-1998 (Rel. 37, Last annotation update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toxin 1 precursor (Toxin II.14) (Cn1).
OS Centruroides noxius (Mexican scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butidae; Butioidae; Butidae; Centruroides.
OX NCBI_TaxID=6878;
RN [1]
RP SEQUENCE FROM N.A., AND AMIDATION.
RX MEDLINE=96119048; PubMed=8585086; DOI=10.1016/0041-0101(95)00058-T;
RA Vazquez A., Tapia J.V., Eliason W.K., Martin B.M., Lebreton F.,
RA Desplegrie M., Posaant L.D., Becerril B.;
RT "Cloning and characterization of the cDNAs encoding Na+ channel-
specific toxins 1 and 2 of the scorpion Centruroides noxius
Hoffmann.";
RL Toxicon 33:1161-1170(1995).
RN [2]
RP SEQUENCE OF 20-84.
RC TISSUE=Venom;
RX MEDLINE=86025386; PubMed=4052021;
RA Posaant L.D.S., Martin B.M., Svendsen I., Rode G.S., Erickson B.W.;
RT "Scorpion toxins from Centruroides noxius and Tityus serrulatus:
primary structures and sequence comparison by metric analysis.";
RL Biochem. J. 229:739-750(1985).
CC -1- FUNCTION: Binds voltage-independently at site 4 of sodium channels
and shift the voltage of activation toward more negative
potentials.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family. Beta-
toxin subfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL; S81093; AAB36085.2; -.
DR PIR; S32789; S32789.
DR HSSP; P01491; 1B3C.

DR InterPro; IPR001219; Neurotoxin.
DR InterPro; IPR02061; Scorpion_toxinL.
DR Pfam; PF00537; Toxin_3; 1.

DR PRINTS; PR00285; SCORPNTOXIN.
DR PRINTS; PR00284; TOXIN.

DR ProDom; PD00908; Scorpion_toxinL; 1.
KW Amdatoin; Direct protein sequencing; Ionic channel inhibitor;
KW Neurotoxin; Signal; Sodium channel inhibitor; Toxin.

FT CHAIN 1 19
FT SIGNAL 1 19
FT DISULFID 20 84 Toxin 1.
FT DISULFID 30 83 By similarity.
FT DISULFID 34 59 By similarity.
FT DISULFID 43 64 By similarity.
FT DISULFID 47 66 By similarity.
FT MOD RES 84 84 Serine amide (G-85 provides amide group).
FT CONFLICT 79 79 P -> T (in Ref. 2).

FT CONFLICT 79 79
SQ SEQUENCE 86 AA; 9586 MW; AB8C1EA742F17222 CRC64;

Query Match 42.1%; Score 51; DB 1; Length 86;
Best Local Similarity 47.4%; Pred. No. 21;
Matches 9; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

OY 4 CYRKYC---GYCRKCR 18
DB 30 CKKCKYKLGKNDYCNRCR 48

RESULT 13

ID Q6ZZP9 PRELIMINARY; PRT; 83 AA.

AC Q6ZZP9; 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative trypsin inhibitor 3.
GN Name=ATT13; ORFNames=At2g43530;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;

RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Leaf;
RX PubMed=15082560; DOI=10.1534/genetics.166.3.1419;

RA Claus M.J., Mitchell-Olds T.;
RT "Functional divergence in tandemly duplicated Arabidopsis thaliana
RT trypsin inhibitor.";

RL Genetics 166:1419-1436(2004).
DR EMBL; AJ632259; CAG15205.1; -.

DR EMBL; AJ632250; CAG15157.1; -.

DR HSSP; Q42328; 1JYC.

DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.

DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR001542; Defense_in_amped.
DR InterPro; IPR003614; Knot1.
DR InterPro; IPR002061; Scorpion_toxinL.

DR Pfam; PF00537; Toxin_3; 1.
DR SMART; SM00505; Knot1; 1.

DR PROSITE; PS00425; ARTHROPOD DEFENSINS; UNKNOWN 1.
SQ SEQUENCE 83 AA; 9408 MW; AV130584F290F934 CRC64;

Query Match 41.3%; Score 50; DB 2; Length 83;
Best Local Similarity 43.8%; Pred. No. 28;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 3 WCYRKYGYCYRKR 18
DB 43 YCMARIYPSLCYRNCR 58

RESULT 14

ID Q6ZZQ4 PRELIMINARY; PRT; 83 AA.

AC Q6ZZQ4; 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative trypsin inhibitor 3.
GN Name=ATT13; ORFNames=At2g43530;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;

RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Leaf;
RX PubMed=15082560; DOI=10.1534/genetics.166.3.1419;

RA Claus M.J., Mitchell-Olds T.;
RT "Functional divergence in tandemly duplicated Arabidopsis thaliana
RT trypsin inhibitor.";

RL Genetics 166:1419-1436(2004).
DR EMBL; AJ632258; CAG15200.1; -.

DR HSSP; Q42328; 1JYC.

DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.

DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR001542; Defense_in_amped.
DR InterPro; IPR003614; Knot1.
DR InterPro; IPR002061; Scorpion_toxinL.

DR Pfam; PF00537; Toxin_3; 1.

DR SMART; SM00505; Knot1; 1.
DR PROSITE; PS00425; ARTHROPOD DEFENSINS; UNKNOWN 1.

SQ SEQUENCE 83 AA; 9424 MW; BDA24E6A1290F93E CRC64;

Query Match 41.3%; Score 50; DB 2; Length 83;
Best Local Similarity 43.8%; Pred. No. 28;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 3 WCYRKYGYCYRKR 18
DB 43 YCMARIYPSLCYRNCR 58

RESULT 15

ID Q6ZZQ9 PRELIMINARY; PRT; 83 AA.

AC Q6ZZQ9; 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative trypsin inhibitor 3.
GN Name=ATT13; ORFNames=At2g43530;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;

RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Leaf;
RX PubMed=15082560; DOI=10.1534/genetics.166.3.1419;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 9, 2005, 20:58:48 ; Search time 164 Seconds
(without alignments)
42.449 Million cell updates/sec

Title: US-10-706-265-2

Perfect score: 121
Sequence: 1 RRCYRCYKCYGCRKCR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq.16Dec04.*

1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	18	2	AAW37578
2	121	100.0	18	2	AAW40570
3	121	100.0	18	2	AAW40561
4	121	100.0	18	2	AAW79839
5	121	100.0	18	4	AAW91844
6	121	100.0	18	8	AD014480
7	121	100.0	19	2	AAW28775
8	121	100.0	19	2	AAW37579
9	121	100.0	19	2	AAW79840
10	118	97.5	18	2	AAW28785
11	118	97.5	18	2	AAW37591
12	118	97.5	18	2	AAW79852
13	117	96.7	18	2	AAW28784
14	117	96.7	18	2	AAW37590
15	117	96.7	18	2	AAW79851
16	116	95.9	17	2	AAW28793
17	116	95.9	17	2	AAW37603
18	116	95.9	17	2	AAW79864
19	116	95.9	18	2	AAW79843
20	115	95.0	18	2	AAW28781
21	115	95.0	18	2	AAW28792
22	115	95.0	18	2	AAW37586
23	115	95.0	18	2	AAW79847
24	115	95.0	18	2	AAW79863
25	114	94.2	18	2	AAW28799

26	114	94.2	18	2	AAW37610
27	114	94.2	18	2	AAW79871
28	113	93.4	17	2	AAW37592
29	113	93.4	17	2	AAW79853
30	113	93.4	18	2	AAW22535
31	113	93.4	18	2	AAW22536
32	113	93.4	18	2	AAW37565
33	113	93.4	18	2	AAW37563
34	113	93.4	18	2	AAW37597
35	113	93.4	18	2	AAW40566
36	113	93.4	18	2	AAW40565
37	113	93.4	18	2	AAW79858
38	113	93.4	18	2	AAW79826
39	113	93.4	18	2	AAW79824
40	113	93.4	19	2	AAW28789
41	113	93.4	19	2	AAW37599
42	113	93.4	19	2	AAW79860
43	112	92.6	17	2	AAW37580
44	112	92.6	17	2	AAW79841
45	112	92.6	18	2	AAW28776

ALIGNMENTS

RESULT 1
ID AAW37578 standard; peptide, 18 AA.
AC AAW37578;
DT 10-MAR-1998 (first entry)
XX
DE Synergistic HIV enzyme inhibitor enhancing peptide (23).
XX
KW Human immunodeficiency virus; HIV; reverse transcriptase; protease;
KW inhibitor; antiviral; synergistic enhancer.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 4..17
FT /note= "optional"
FT Modified-site 18
FT /note= "amidated"
XX
PN JP09025240-A.
XX
PD 28-JAN-1997.
XX
PF 11-JUL-1995; 95JP-00197129.
XX
PR 11-JUL-1995; 95JP-00197129.
XX
PA (SEKK) SEIKAGAKU KOGYO CO LTD.
XX
WP; 1997-149771/14.
DR
XX
PT Antiviral compsn. against human immunodeficiency virus - contg. specified
PT polypeptide and HIV reverse transcriptase inhibitor or HIV protease
PT inhibitor.
XX
PS Example; Page 6; 13pp; Japanese.
XX
CC A novel medicinal composition, comprising the present peptide and a human
CC immunodeficiency virus (HIV) reverse transcriptase or protease inhibitor,
CC can be used as an antiviral drug. The composition is highly active
CC against HIV, and can be administered over a long period. The dose of the
CC HIV enzyme inhibitor can be reduced, because combined use with the
CC present peptide synergistically enhances its antiviral activity
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 121; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCRYRCKYKGYCYRCKR 18
DB 1 RRMCRYRCKYKGYCYRCKR 18

RESULT 2

AAW40570 ID AAW40570 standard; peptide; 18 AA.

AC AAW40570;

DT 27-AUG-1998 (first entry)

DE Polypeptide transition metal peptide fragment.

XX Polypeptide transition metal salt; inhibition; viral activity; HIV.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "labelled with FTC"

XX W09816555-A1.

PD 23-APR-1998.

PF 15-OCT-1997; 97WO-JP003711.

PR 15-OCT-1996; 96JP-00291215.

PA (SEBK) SEIKAGAKU CORP.

PI Matsumoto A, Waki M;

DR WPI; 1998-251233/22.

XX Polypeptide transition metal salt or its acid adduct - useful for
inhibiting viral activity, e.g. HIV in vivo.

PS Disclosure; Page 6; 45pp; Japanese.

XX AAW40561-70 represent fragments of a polypeptide transition metal salt or
its acid adduct. The peptides comprise the formula: A1-A2-Cys-A2-A3-A3-X-
Y-Z-A2-A3-A3-Cys-A3-A4 where A1 = Lys, Arg or Orn, optionally N- alpha
substituted or peptide comprising at least 2 of these residues,
or optionally N- alpha substituted; A2 = Phe, Trp or Tyr; A3 = Arg, Lys or
Orn; A4 = -OH or -NH2; X = dipeptide comprising Ala, Val, Leu, Ile, Ser,
Met or Cys bound to A1; Y = dipeptide comprising Gly and A3 or Pro, D-
Arg, D-Lys or D-Orn, and Z = dipeptide comprising Ala, Val, Leu, Ile,
Ser, Met or A2 bound to Cys, or the peptide bond linked X-Y-Z have
peptide bonds to other aa at positions 6 and 10, or if neither X nor Z
exist, then Y may bond to them directly, in which case the D-Lys, L-Lys,
D-Orn or L-Orn of Y may be substituted by omega-aminoacyl. The salt may
be used for inhibiting viral activity, and is especially useful against
HIV in vivo

CC Sequence 18 AA;

Query Match 100.0%; Score 121; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCRYRCKYKGYCYRCKR 18
DB 1 RRMCRYRCKYKGYCYRCKR 18

RESULT 3

AAW40561 ID AAW40561 standard; peptide; 18 AA.

AC AAW40561;

DT 27-AUG-1998 (first entry)

DE Polypeptide transition metal peptide fragment.

XX Polypeptide transition metal salt; inhibition; viral activity; HIV.

OS Synthetic.

XX W09816555-A1.

PD 23-APR-1998.

PF 15-OCT-1997; 97WO-JP003711.

PR 15-OCT-1996; 96JP-00291215.

PA (SEBK) SEIKAGAKU CORP.

PI Matsumoto A, Waki M;

DR WPI; 1998-251233/22.

XX Polypeptide transition metal salt or its acid adduct - useful for
inhibiting viral activity, e.g. HIV in vivo.

PS Disclosure; Page 6; 45pp; Japanese.

XX AAW40561-70 represent fragments of a polypeptide transition metal salt or
its acid adduct. The peptides comprise the formula: A1-A2-Cys-A2-A3-A3-X-
Y-Z-A2-A3-A3-Cys-A3-A4 where A1 = Lys, Arg or Orn, optionally N- alpha
substituted or peptide comprising at least 2 of these residues,
or optionally N- alpha substituted; A2 = Phe, Trp or Tyr; A3 = Arg, Lys or
Orn; A4 = -OH or -NH2; X = dipeptide comprising Ala, Val, Leu, Ile, Ser,
Met or Cys bound to A1; Y = dipeptide comprising Gly and A3 or Pro, D-
Arg, D-Lys or D-Orn, and Z = dipeptide comprising Ala, Val, Leu, Ile,
Ser, Met or A2 bound to Cys, or the peptide bond linked X-Y-Z have
peptide bonds to other aa at positions 6 and 10, or if neither X nor Z
exist, then Y may bond to them directly, in which case the D-Lys, L-Lys,
D-Orn or L-Orn of Y may be substituted by omega-aminoacyl. The salt may
be used for inhibiting viral activity, and is especially useful against
HIV in vivo

CC Sequence 18 AA;

Query Match 100.0%; Score 121; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCRYRCKYKGYCYRCKR 18
DB 1 RRMCRYRCKYKGYCYRCKR 18

RESULT 4

AAW79839 ID AAW79839 standard; peptide; 18 AA.

AC AAW79839;

DT 08-DEC-1998 (first entry)

DE Peptide sequence of the specification.

XX Reverse-transcriptase inhibitor; HIV protease inhibitor;

KW HIV surface protein gp120; cell surface protein CD4; treatment; AIDS;

OS AIDS-associated syndrome.
Synthetic.

XX MO9843995-A1.
XX 08-OCT-1998.
XX 26-MAR-1998; 98WO-JP001366.
XX 28-MAR-1997; 97JP-00092801.
XX (SEK) SEIKAGAKU CORP.
XX Fujii N;
XX WPI; 1998-542630/46.
XX New therapeutic compositions comprise anti-HIV complexes - useful for
PT homing drug substance to target cells to enhance anti-HIV activity, for
PT treatment of AIDS.
XX Disclosure; Page 10; 44pp; Japanese.
XX AA079817-85 appear in the specification. The specification describes
CC complexes which comprise at least one reverse-transcriptase inhibitor
CC and/or HIV protease inhibitor chemically bonded to polypeptides with an
CC affinity for HIV surface protein gp120 and/or HIV host target cell
CC surface protein CD4. The complexes can be used to prepare therapeutics
CC for treatment of AIDS and AIDS-associated syndromes
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 121; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRMCRYRCKYKGYCYRCKR 18
DB 1 RRMCRYRCKYKGYCYRCKR 18
RESULT 5
AAB91844
ID AAB91844 standard; peptide; 18 AA.
XX
AC AAB91844;
XX
DT 22-JUN-2001 (first entry)
XX
DE Antimicrobial peptide SEQ ID NO:1020.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimide; maleimide group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1998; 98US-0134406P.
PR 10-SEP-1998; 98US-0134406P.
PR 15-OCT-1998; 98US-0134406P.
XX
PA (CONT-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 529; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (II) and a
CC reactive group (III) (e.g. succinimide) and maleimide groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilized therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 121; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRMCRYRCKYKGYCYRCKR 18
DB 1 RRMCRYRCKYKGYCYRCKR 18
RESULT 6
ADQ14480
ID ADQ14480 standard; peptide; 18 AA.
XX
AC ADQ14480;
XX
DT 23-SEP-2004 (first entry)
XX
DE Metastasis inhibiting peptide seqid 2.
XX
KM Metastasis; tumour; CXC Chemokine Receptor-4; CXCR4; breast cancer;
KM breast tumour; lymphoma; neuroblastoma; lung cancer; angiosarcoma;
KM pancreatic cancer; leukaemia; prostate cancer.
XX
OS Synthetic.
XX
PN US2004132642-A1.
XX
PD 08-JUL-2004.
XX
PF 12-NOV-2003; 2003US-00706265.
XX
PR 12-NOV-2002; 2002US-0425472P.
PR 15-OCT-2003; 2003US-0511581P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Hwang S;
XX
DR WPI; 2004-517028/49.
XX
PT Use of a polypeptide that inhibits metastasis of tumor cells, which
PT expresses CXC Chemokine Receptor-4, for inhibiting metastasis or growth
PT of a tumor cell.
XX
PS Claim 2; SEQ ID NO 2; 31pp; English.
XX
CC The invention describes the use of a polypeptide that inhibits metastasis
CC of tumour cells, where the tumour cell expresses CXC Chemokine Receptor-4
CC (CXCR4), for inhibiting metastasis or growth of a tumor cell. Also

CC described are: inhibiting metastasis of a tumour cell in a mammal; and
 CC inhibiting growth of a tumour cell. The polypeptide is useful for
 CC inhibiting metastasis or growth of a tumour cell. The tumour cell is a
 CC breast cancer cell, a breast tumour cell, a lymphoma cell, a
 CC neuroblastoma cell, a lung cancer cell, an angiosarcoma cell, a
 CC pancreatic cancer cell, a leukaemia cell, or a prostate cancer cell. This
 CC is the amino acid sequence of peptide that can be used to inhibit
 CC metastasis in tumour cells.

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 121; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRMCYRCKYKGYCKR 18
 DB 1 RRMCYRCKYKGYCKR 18

RESULT 7

AAW37579 standard; peptide; 19 AA.

XX AAR28775;

XX 25-MAR-2003 (revised)

DT 23-MAR-1993 (first entry)

XX High endotoxin affinity polypeptide.

XX Lipopolysaccharide affinity; tachyplesin-like; polyphemusin-like;

KM antiviral activity; HIV, human immunodeficiency virus.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 19

FT /note= "Arg-NH2"

XX EPI13613-A1.

XX 19-NOV-1992.

XX 04-MAY-1992; 92EP-00107509.

XX 02-MAY-1991; 91JP-00130410.

XX (SEBK) SEIKAGAKU KOGYO CO LTD.

XX Fujii N, Yamamoto N, Matsumoto A, Waki M;

XX WPI; 1992-383533/47.

XX New tachyplesin- and polyphemusin-like polypeptide(s) - have endotoxin-
 PT binding activity, antibacterial activity and antiviral activity, partic.
 PT anti-HIV activity.

XX Disclosure; Page 4; 17pp; English.

XX The polypeptide has an ability to bind endotoxins, an antibacterial
 CC activity and an activity to haemolyse endotoxin-sensitised haemocytes. It
 CC also has antiviral activity, specifically anti-HIV activity. It exhibits
 CC higher anti-HIV activity than known related high endotoxin affinity
 CC polypeptides, e.g. tachyplesins I, II or III or polyphemusins I or II. It
 CC may be prepd. by solid phase synthesis or recombinant DNA techniques.
 CC Opt. the Cys residues at positions 4 and 17 are linked through a
 CC disulphide linkage as are the Cys residues at positions 8 and 13. See
 CC also AAR28775-R28799 and AAR28804. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 19 AA;

Query Match 100.0%; Score 121; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRMCYRCKYKGYCKR 18
 DB 1 RRMCYRCKYKGYCKR 18

RESULT 8

AAW37579 standard; peptide; 19 AA.

XX AAW37579;

XX 10-MAR-1998 (first entry)

XX Synergistic HIV enzyme inhibitor enhancing peptide (24).

KM Human immunodeficiency virus; HIV; reverse transcriptase; protease;
 XX inhibitor; antiviral; synergistic enhancer.

OS Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 4..17

FT /note= "optional"

FT Modified-site 19

FT /note= "amidated"

XX JPO9025240-A.

XX 28-JAN-1997.

XX 11-JUL-1995; 95JP-00197129.

XX 11-JUL-1995; 95JP-00197129.

XX (SEBK) SEIKAGAKU KOGYO CO LTD.

XX WPI; 1997-149771/14.

XX Antiviral compsn. against human immunodeficiency virus - contg. specified
 PT polypeptide and HIV reverse transcriptase inhibitor or HIV protease
 PT inhibitor.

XX Example; Page 6; 13pp; Japanese.

XX A novel medicinal composition, comprising the present peptide and a human
 CC immunodeficiency virus (HIV) reverse transcriptase or protease inhibitor,
 CC can be used as an antiviral drug. The composition is highly active
 CC against HIV, and can be administered over a long period. The dose of the
 CC HIV enzyme inhibitor can be reduced because combined use with the
 CC present peptide synergistically enhances its antiviral activity

XX Sequence 19 AA;

Query Match 100.0%; Score 121; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRMCYRCKYKGYCKR 18
 DB 1 RRMCYRCKYKGYCKR 18

RESULT 9

AAW79840 standard; peptide; 19 AA.

XX AAW79840;

XX 08-DEC-1998 (first entry)

PS Example; Page 7; 13pp; Japanese.

XX A novel medicinal composition, comprising the present peptide and a human
CC immunodeficiency virus (HIV) reverse transcriptase or protease inhibitor,
CC can be used as an antiviral drug. The composition is highly active
CC against HIV, and can be administered over a long period. The dose of the
CC HIV enzyme inhibitor can be reduced, because combined use with the
CC present peptide synergistically enhances its antiviral activity
XX

Sequence 18 AA;

Query Match 97.5%; Score 118; DB 2; Length 18;
Best Local Similarity 94.4%; Pred. No. 4e-07;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRMCRYRCKYKGYCYRKR 18
DB 1 RRMCRYRCKYRGGYCYRKR 18

RESULT 12

AAW79852
ID AAW79852 standard; peptide; 18 AA.

XX AAW79852;

DT 08-DEC-1998 (first entry)

DE Peptide sequence of the specification.

XX Reverse-transcriptase inhibitor; HIV protease inhibitor;

KW HIV surface protein gp120; cell surface protein CD4; treatment; AIDS;

KW AIDS-associated syndrome.

XX Synthetic.

XX WO9843995-A1.

PD 08-OCT-1998.

PF 26-MAR-1998; 98WO-JP001366.

PR 28-MAR-1997; 97JP-00092801.

PA (SEGG) SEIKAGAKU CORP.

PI Fujii N;

DR WPI; 1998-542630/46.

XX New therapeutic compositions comprise anti-HIV complexes - useful for
PT homing drug substance to target cells to enhance anti-HIV activity, for
PT treatment of AIDS.

XX Disclosure; Page 11; 44pp; Japanese.

CC AAW79817-85 appear in the specification. The specification describes
CC complexes which comprise at least one reverse-transcriptase inhibitor
CC and/or HIV protease inhibitor chemically bonded to polypeptides with an
CC affinity for HIV surface protein gp120 and/or HIV host target cell
CC surface protein CD4. The complexes can be used to prepare therapeutics
CC for treatment of AIDS and AIDS-associated syndromes
XX

Sequence 18 AA;

Query Match 97.5%; Score 118; DB 2; Length 18;
Best Local Similarity 94.4%; Pred. No. 4e-07;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRMCRYRCKYKGYCYRKR 18
DB 1 RRMCRYRCKYRGGYCYRKR 18

RESULT 13

AAW28784
ID AAW28784 standard; peptide; 18 AA.

XX AAW28784;

DT 25-MAR-2003 (revised)

DT 23-MAR-1993 (first entry)

XX High endotoxin affinity polypeptide.

KW Lipopolysaccharide affinity; tachyplesin-like; polymyxin-like;
XX antiviral activity; HIV; human immunodeficiency virus.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 18 /note= "Arg-NH2"

XX EP513613-A1.

PD 19-NOV-1992.

PF 04-MAY-1992; 92EP-00107509.

PR 02-MAY-1991; 91JP-00130410.

PA (SEGG) SEIKAGAKU KOGYO CO LTD.

PI Fujii N, Yamamoto N, Matsumoto A, Waki M;

XX WPI; 1992-383533/47.

XX New tachyplesin- and polymyxin-like polypeptide(s) - have endotoxin-
PT binding activity, antibacterial activity and antiviral activity, partic.
PT anti-HIV activity.

XX Disclosure; Page 4; 17pp; English.

CC The polypeptide has an ability to bind endotoxins, an antibacterial
CC activity and an activity to haemolyse endotoxin-sensitized haemocytes. It
CC also has antiviral activity, specifically anti-HIV activity. It exhibits
CC higher anti-HIV activity than known related high endotoxin affinity
CC polypeptides, e.g. Tachyplesins I, II or III or polymyxins I or II. It
CC may be prepd. by solid phase synthesis or recombinant DNA techniques.
CC Opt. the Cys residues at positions 4 and 17 are linked through a
CC disulphide linkage as are the Cys residues at positions 8 and 13. See
CC also AAW28775-R28799 and AAW28804. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX

Sequence 18 AA;

Query Match 96.7%; Score 117; DB 2; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.2e-07;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRMCRYRCKYKGYCYRKR 18
DB 1 RRMCRYRCKYRGGYCYRKR 18

RESULT 14

AAW37590
ID AAW37590 standard; peptide; 18 AA.

XX AAW37590;

DT 10-MAR-1998 (first entry)

XX Synergistic HIV enzyme inhibitor enhancing peptide (35).
DE
XX

KV Human immunodeficiency virus; HIV, reverse transcriptase; protease;
 KW inhibitor; antiviral; synergistic enhancer.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Disulfide-bond 4..17
 FT /note= "optional"
 FT Modified-site 18
 FT /note= "amidated"
 XX
 XX JP09025240-A.
 XX
 XX 28-JAN-1997.
 XX
 XX 11-JUL-1995; 95JP-00197129.
 XX
 XX 11-JUL-1995; 95JP-00197129.
 XX
 XX (SEKG) SEIKAGAKU KOGYO CO LTD.
 XX
 XX WPI; 1997-149771/14.
 XX
 XX Antiviral compsn. against human immunodeficiency virus - contg. specified
 PT polypeptide and HIV reverse transcriptase inhibitor or HIV protease
 PT inhibitor.
 XX
 XX Example; Page 7; 13pp; Japanese.
 XX
 CC A novel medicinal composition, comprising the present peptide and a human
 CC immunodeficiency virus (HIV) reverse transcriptase or protease inhibitor,
 CC can be used as an antiviral drug. The composition is highly active
 CC against HIV, and can be administered over a long period. The dose of the
 CC HIV enzyme inhibitor can be reduced, because combined use with the
 CC present peptide synergistically enhances its antiviral activity
 XX
 SQ Sequence 18 AA;
 Query Match 96.7%; Score 117; DB 2; Length 18;
 Best Local Similarity 94.4%; Pred. No. 5.2e-07;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRMCTRKCKYKGYCKRKR 18
 1 RRMCTRKCKYKGYCKRKR 18
 DB 1 RRMCTRKCKYKGYCKRKR 18
 RESULT 15
 AAM79851
 ID AAM79851 standard; peptide; 18 AA.
 XX
 AC AAM79851;
 XX
 DT 08-DEC-1998 (first entry)
 XX
 DE Peptide sequence of the specification.
 XX
 KW Reverse-transcriptase inhibitor; HIV protease inhibitor;
 KW HIV surface protein gp120; cell surface protein CD4; treatment; AIDS;
 KM AIDS-associated syndrome.
 XX
 OS Synthetic.
 XX
 XX WO9843995-A1.
 XX
 XX 08-OCT-1998.
 XX
 XX 26-MAR-1998; 98WO-JP001366.
 XX
 XX 28-MAR-1997; 97JP-00092801.
 XX
 XX (SEKG) SEIKAGAKU CORP.
 XX

PI Fujii N;
 XX
 XX WPI; 1998-542630/46.
 DR
 XX
 XX New therapeutic compositions comprise anti-HIV complexes - useful for
 PT homing drug substance to target cells to enhance anti-HIV activity, for
 PT treatment of AIDS.
 XX
 XX Disclosure; Page 11; 44pp; Japanese.
 XX
 XX AAM79817-85 appear in the specification. The specification describes
 CC complexes which comprise at least one reverse-transcriptase inhibitor
 CC and/or HIV protease inhibitor chemically bonded to polypeptides with an
 CC affinity for HIV surface protein gp120 and/or HIV host target cell
 CC surface protein CD4. The complexes can be used to prepare therapeutics
 CC for treatment of AIDS and AIDS-associated syndromes
 XX
 SQ Sequence 18 AA;
 Query Match 96.7%; Score 117; DB 2; Length 18;
 Best Local Similarity 94.4%; Pred. No. 5.2e-07;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 1 RRMCTRKCKYKGYCKRKR 18
 DB 1 RRMCTRKCKYKGYCKRKR 18
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 Job time : 165 secs

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OW protein - protein search, using sw model

Run on: May 9, 2005, 21:07:54 ; Search time 42 Seconds
(without alignments)
31.992 Million cell updates/sec

Title: US-10-706-265-2

Perfect score: 121
Sequence: 1 RRMCKYKCYKCR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	121	100.0	18 1 US-07-876-883-7	Sequence 7, Appli
2	121	100.0	18 1 US-08-426-550-7	Sequence 7, Appli
3	121	100.0	18 3 US-09-284-241-1	Sequence 1, Appli
4	121	100.0	19 1 US-07-876-883-8	Sequence 8, Appli
5	121	100.0	19 1 US-08-426-550-8	Sequence 8, Appli
6	118	97.5	18 1 US-07-876-883-20	Sequence 20, Appli
7	118	97.5	18 1 US-08-426-550-20	Sequence 20, Appli
8	117	96.7	18 1 US-07-876-883-19	Sequence 19, Appli
9	117	96.7	18 1 US-08-426-550-19	Sequence 19, Appli
10	116	95.9	17 1 US-07-876-883-32	Sequence 32, Appli
11	116	95.9	17 1 US-08-426-550-32	Sequence 32, Appli
12	115	95.0	18 1 US-07-876-883-15	Sequence 15, Appli
13	115	95.0	18 1 US-07-876-883-31	Sequence 15, Appli
14	115	95.0	18 1 US-08-426-550-15	Sequence 15, Appli
15	115	95.0	18 1 US-08-426-550-31	Sequence 31, Appli
16	114	94.2	18 1 US-07-876-883-39	Sequence 39, Appli
17	114	94.2	18 1 US-08-426-550-39	Sequence 39, Appli
18	113	93.4	17 1 US-07-876-883-21	Sequence 21, Appli
19	113	93.4	17 1 US-08-426-550-21	Sequence 21, Appli
20	113	93.4	18 1 US-07-876-883-26	Sequence 26, Appli
21	113	93.4	18 1 US-07-856-026B-9	Sequence 9, Appli
22	113	93.4	18 1 US-07-856-026B-11	Sequence 11, Appli
23	113	93.4	18 1 US-08-426-550-26	Sequence 26, Appli
24	113	93.4	18 3 US-09-284-241-4	Sequence 4, Appli
25	113	93.4	19 1 US-07-876-883-28	Sequence 28, Appli
26	113	93.4	19 1 US-08-426-550-28	Sequence 28, Appli
27	112	92.6	17 1 US-07-876-883-9	Sequence 9, Appli

28	112	92.6	17 1 US-08-426-550-9	Sequence 9, Appli
29	112	92.6	18 1 US-07-876-883-10	Sequence 10, Appli
30	112	92.6	18 1 US-08-426-550-10	Sequence 10, Appli
31	112	92.6	19 1 US-07-876-883-14	Sequence 14, Appli
32	112	92.6	19 1 US-08-426-550-14	Sequence 14, Appli
33	111	91.7	16 1 US-07-876-883-33	Sequence 33, Appli
34	111	91.7	16 1 US-08-426-550-33	Sequence 33, Appli
35	111	91.7	18 1 US-07-876-883-11	Sequence 11, Appli
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37	110	90.9	18 1 US-07-876-883-22	Sequence 22, Appli
38	110	90.9	18 1 US-07-856-026B-4	Sequence 4, Appli
39	110	90.9	18 1 US-07-856-026B-6	Sequence 6, Appli
40	110	90.9	18 1 US-08-426-550-22	Sequence 22, Appli
41	110	90.9	18 3 US-09-284-241-3	Sequence 3, Appli
42	109	90.1	17 1 US-07-876-883-25	Sequence 25, Appli
43	109	90.1	17 1 US-08-426-550-25	Sequence 25, Appli
44	109	90.1	18 1 US-07-876-883-18	Sequence 18, Appli
45	109	90.1	18 1 US-08-426-550-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-07-876-883-7
; Sequence 7, Application US/07876883
; Patent No. 5449752
; GENERAL INFORMATION:
; APPLICANT: Fujii, No. 5449752utaka
; APPLICANT: Yamamoto, Naoki
; APPLICANT: Matsumoto, Akiyoshi
; APPLICANT: Maki, Michinori
; TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
; TITLE OF INVENTION: Lipopolysaccharides And Their Uses
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/876, 883
; FILING DATE: 19920429
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Charles E.
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 7568-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-9741
; TELELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-07-876-883-7
; Query Match 100.0%; Score 121; DB 1; Length 18;
; Best Local Similarity 100.0%; Pred. No. 1e-08;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRMCKYKCYKCR 18

Db 1 RRMCRYKCYKGYCYRKCR 18

RESULT 2

US-08-426-550-7
; Sequence 7, Application US/08426550
; Patent No. 5710128
; GENERAL INFORMATION:
; APPLICANT: Fujii, No. 5710128utaka
; APPLICANT: Yamamoto, Naoki
; APPLICANT: Matsumoto, Akiyoshi
; APPLICANT: Waki, Michinori
; TITLE OF INVENTION: Pharmaceutical Compositions of
; TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,550
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Charles E.
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 7568-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO. 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-426-550-7

Query Match 100.0%; Score 121; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCRYKCYKGYCYRKCR 18
Db 1 RRMCRYKCYKGYCYRKCR 18

RESULT 3
US-09-284-241-1
; Sequence 1, Application US/09284241B
; Patent No. 6329498
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, AKIYOSHI
; APPLICANT: WAKI, MICHINORI
; TITLE OF INVENTION: POLYPEPTIDE TRANSITION METAL SALTS AND METHOD OF
; TITLE OF INVENTION: ENHANCING ANTI-HIV ACTIVITY OF POLYPEPTIDE
; FILE REFERENCE: 9378-0005-0PCT
; CURRENT APPLICATION NUMBER: US/09/284,241B
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: PCT/JP97/03711
; EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-284-241-1

Query Match 100.0%; Score 121; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCRYKCYKGYCYRKCR 18
Db 1 RRMCRYKCYKGYCYRKCR 18

RESULT 4

US-07-876-883-8
; Sequence 8, Application US/07876883
; Patent No. 5449752
; GENERAL INFORMATION:
; APPLICANT: Fujii, No. 5449752utaka
; APPLICANT: Yamamoto, Naoki
; APPLICANT: Matsumoto, Akiyoshi
; APPLICANT: Waki, Michinori
; TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
; TITLE OF INVENTION: Lipopolysaccharides And Their Uses
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/876,883
; FILING DATE: 19920429
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Charles E.
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 7568-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO. 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-07-876-883-8

Query Match 100.0%; Score 121; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCRYKCYKGYCYRKCR 18
Db 1 RRMCRYKCYKGYCYRKCR 18

RESULT 5

US-08-426-550-8
; Sequence 8, Application US/08426550
; Patent No. 5710128
; GENERAL INFORMATION:
; APPLICANT: Fujii, No. 5710128utaka
; APPLICANT: Yamamoto, Naoki
; APPLICANT: Matsumoto, Akiyoshi
; APPLICANT: Waki, Michinori
; TITLE OF INVENTION: Pharmaceutical Compositions of
; TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,550
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Charles E.
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 7568-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-426-550-8

Query Match 100.0%; Score 121; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RRMCRKCYKGYCYRKR 18
Db 1 RRMCRKCYKGYCYRKR 18

RESULT 6
US-07-876-883-20
; Sequence 20, Application US/07876883
; Patent No. 5449752
; GENERAL INFORMATION:
; APPLICANT: Fujii, No. 5449752utaka
; APPLICANT: Yamamoto, Naoki
; APPLICANT: Matsumoto, Akiyoshi
; APPLICANT: Waki, Michinori
; TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
; TITLE OF INVENTION: Lipopolysaccharides And Their Uses
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,883
FILING DATE: 19920429
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-876-883-20

Query Match 97.5%; Score 118; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.4e-08;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RRMCRKCYKGYCYRKR 18
Db 1 RRMCRKCYKGYCYRKR 18

RESULT 7
US-08-426-550-20
; Sequence 20, Application US/08426550
; Patent No. 5710128
; GENERAL INFORMATION:
; APPLICANT: Fujii, No. 5710128utaka
; APPLICANT: Yamamoto, Naoki
; APPLICANT: Matsumoto, Akiyoshi
; APPLICANT: Waki, Michinori
; TITLE OF INVENTION: Pharmaceutical Compositions of
; TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,550
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Charles E.
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 7568-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-426-550-20

Query Match 97.5%; Score 118; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.4e-08;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCRYKCYKGYCYRKCR 18
DB 1 RRMCRYKCYKGYCYRKCR 18

RESULT 8
US-07-876-883-19
Sequence 19, Application US/07876883
Patent No. 5449752
GENERAL INFORMATION:
APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,883
FILING DATE: 19920429
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-876-883-19

Query Match 96.7%; Score 117; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.2e-08;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCRYKCYKGYCYRKCR 18
DB 1 RRMCRYKCYKGYCYRKCR 18

RESULT 9
US-08-426-550-19
Sequence 19, Application US/08426550
Patent No. 5710128

GENERAL INFORMATION:
APPLICANT: Fujii, No. 5710128utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: Pharmaceutical Compositions of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,550
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-426-550-19

Query Match 96.7%; Score 117; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.2e-08;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCRYKCYKGYCYRKCR 18
DB 1 RRMCRYKCYKGYCYRKCR 18

RESULT 10
US-07-876-883-32
Sequence 32, Application US/07876883
Patent No. 5449752
GENERAL INFORMATION:
APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,883
FILING DATE: 19920429
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-876-883-32

Query Match 95.9%; Score 116; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RWCYRKCYKGYCYRKCR 18
Db 1 RWCYRKCYKGYCYRKCR 17

RESULT 11
US-08-426-550-32
Sequence 32, Application US/08426550
Patent No. 5710128
GENERAL INFORMATION:
APPLICANT: Fujii, No. 5710128utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
TITLE OF INVENTION: Pharmaceutical Compositions of
Lipopolysaccharide-Binding Polypeptides
NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,550
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown

MOLECULE TYPE: peptide
US-08-426-550-32

Query Match 95.9%; Score 116; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RWCYRKCYKGYCYRKCR 18
Db 1 RWCYRKCYKGYCYRKCR 17

RESULT 12
US-07-876-883-15
Sequence 15, Application US/07876883
Patent No. 5449752
GENERAL INFORMATION:
APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
Lipopolysaccharides And Their Uses
NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,883
FILING DATE: 19920429
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-876-883-15

Query Match 95.0%; Score 115; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.5e-08;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RWCYRKCYKGYCYRKCR 18
Db 1 RWCYRKCYKGYCYRKCR 18

RESULT 13
US-07-876-883-31
Sequence 31, Application US/07876883
Patent No. 5449752
GENERAL INFORMATION:
APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Yamamoto, Naoki

APPLICANT: Matsumoto, Akiyoshi
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-876-883-31

Query Match 95.0%; Score 115; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.5e-08;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCRYKCYKGYCKR 18
DB 1 RRMCRYKCYKGYCKR 18

RESULT 14
US-08-426-550-15
Sequence 15, Application US/08426550
Patent No. 5710128
GENERAL INFORMATION:
APPLICANT: Fujii, No. 5710128utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: Pharmaceutical Compositions of
Lipopolysaccharide-Binding Polypeptides
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,550

FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-426-550-15

Query Match 95.0%; Score 115; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.5e-08;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMCRYKCYKGYCKR 18
DB 1 RRMCRYKCYKGYCKR 18

RESULT 15
US-08-426-550-31
Sequence 31, Application US/08426550
Patent No. 5710128
GENERAL INFORMATION:
APPLICANT: Fujii, No. 5710128utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: Pharmaceutical Compositions of
Lipopolysaccharide-Binding Polypeptides
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,550
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-426-550-31

Query Match 95.0%; Score 115; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. NO. 5.5e-08;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRMCTRRCKGKCYRKR 18
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| | | | | : | | | | | : | |
Db 1 RRMCTRRCKGKCYRKR 18

Search completed: May 9, 2005, 21:15:59
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: May 9, 2005, 21:08:50 ; Search time 133 Seconds
(without alignments)
45.149 Million cell updates/sec

Title: US-10-706-265-2

Perfect score: 121
Sequence: 1 RRMCKRYKCYKCR 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1428581 seqs, 333598853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications RA:*

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- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
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- 16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep:*
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- 20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	121	100.0	18	16	US-10-706-265-2	Sequence 2, Appl1
2	106	87.6	18	9	US-09-030-619-220	Sequence 220, App
3	106	87.6	18	9	US-09-912-609-108	Sequence 108, App
4	106	87.6	18	15	US-10-277-232-220	Sequence 220, App
5	106	87.6	18	15	US-10-277-233-820	Sequence 220, App
6	106	87.6	18	17	US-10-838-289-744	Sequence 744, App
7	103	85.1	18	9	US-09-030-619-219	Sequence 219, App
8	103	85.1	18	9	US-09-912-609-107	Sequence 107, App
9	103	85.1	18	13	US-10-042-872-13	Sequence 13, Appl1
10	103	85.1	18	15	US-10-277-232-219	Sequence 219, App
11	103	85.1	18	15	US-10-277-233-219	Sequence 219, App
12	103	85.1	18	17	US-10-838-289-743	Sequence 743, App
13	96	79.3	18	13	US-10-042-872-18	Sequence 18, Appl1

14	95	78.5	18	13	US-10-042-872-10	Sequence 10, Appl1
15	94	77.7	17	9	US-09-030-619-229	Sequence 229, App
16	94	77.7	17	9	US-09-912-609-117	Sequence 117, App
17	94	77.7	17	9	US-09-912-609-117	Sequence 117, App
18	94	77.7	17	15	US-10-277-232-229	Sequence 229, App
19	94	77.7	17	15	US-10-277-233-229	Sequence 229, App
20	94	77.7	17	17	US-10-844-837-6	Sequence 6, Appl1
21	94	77.7	17	17	US-10-838-289-753	Sequence 753, App
22	94	77.7	17	17	US-10-909-119-21	Sequence 21, Appl1
23	94	77.7	17	17	US-10-657-851-6	Sequence 6, Appl1
24	92.5	76.4	19	13	US-10-042-872-11	Sequence 11, Appl1
25	92.5	76.4	19	13	US-10-042-872-19	Sequence 19, Appl1
26	90	74.4	18	13	US-10-042-872-1	Sequence 1, Appl1
27	88	72.7	17	9	US-09-030-619-228	Sequence 228, App
28	88	72.7	17	9	US-09-912-609-116	Sequence 116, App
29	88	72.7	17	9	US-09-917-340-5	Sequence 5, Appl1
30	88	72.7	17	13	US-10-042-872-12	Sequence 12, Appl1
31	88	72.7	17	15	US-10-277-232-228	Sequence 228, App
32	88	72.7	17	15	US-10-277-233-228	Sequence 228, App
33	88	72.7	17	17	US-10-844-837-5	Sequence 5, Appl1
34	88	72.7	17	17	US-10-838-289-752	Sequence 752, App
35	88	72.7	17	17	US-10-909-119-20	Sequence 20, Appl1
36	88	72.7	17	17	US-10-657-851-5	Sequence 5, Appl1
37	80	66.1	18	13	US-10-042-872-3	Sequence 3, Appl1
38	79	65.3	18	13	US-10-042-872-5	Sequence 5, Appl1
39	78	64.5	18	13	US-10-042-872-6	Sequence 6, Appl1
40	73	60.3	17	13	US-10-042-872-2	Sequence 2, Appl1
41	73	60.3	18	13	US-10-042-872-16	Sequence 16, Appl1
42	71	58.7	18	13	US-10-042-872-15	Sequence 15, Appl1
43	70	57.9	18	13	US-10-042-872-8	Sequence 8, Appl1
44	70	57.9	18	13	US-10-042-872-9	Sequence 9, Appl1
45	68	56.2	17	15	US-10-360-101-24	Sequence 24, Appl1

ALIGNMENTS

RESULT 1
US-10-706-265-2
Sequence 2, Application US/10706265
Publication No. US20040132642A1
GENERAL INFORMATION:
APPLICANT: Hwang, Sam
TITLE OF INVENTION: METHODS OF INHIBITING METASTASIS OR GROWTH OF A TUMOR CELL
FILE REFERENCE: 224728
CURRENT APPLICATION NUMBER: US/10/706,265
PRIOR FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/425,472
PRIOR FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 60/511,581
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic
US-10-706-265-2

Query Match 100.0%; Score 121; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RRMCKRYKCYKCR 18
|||||
Db 1 RRMCKRYKCYKCR 18

RESULT 2
US-09-030-619-220
Sequence 220, Application US/09030619B

Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTI-BIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,6198
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Limulus polyphemus
US-09-030-619-220

Query Match 87.6%; Score 106; DB 9; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.2e-06;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRMCRKCYKGYCYRKR 18
|||:|||||:
Db 1 RRMCRVCYKGFYRKR 18

RESULT 3
US-09-912-609-108

; Sequence 108, Application US/09912609
; Publication No. US20020041898A1
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUMAGI, TERRY ONICHI
; APPLICANT: VAMADARAJAN
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001.24
; CURRENT APPLICATION NUMBER: US/09/912,609
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 108
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-912-609-108

Query Match 87.6%; Score 106; DB 9; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.2e-06;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRMCRKCYKGYCYRKR 18
|||:|||||:
Db 1 RRMCRVCYKGFYRKR 18

RESULT 4
US-10-277-232-220
; Sequence 220, Application US/10277232
; Publication No. US20030211537A1
; GENERAL INFORMATION:

; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTI-BIOTICS
; FILE REFERENCE: 660081.406C1
; CURRENT APPLICATION NUMBER: US/10/277,232
; CURRENT FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Limulus polyphemus
US-10-277-232-220

Query Match 87.6%; Score 106; DB 15; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.2e-06;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRMCRKCYKGYCYRKR 18
|||:|||||:
Db 1 RRMCRVCYKGFYRKR 18

RESULT 5
US-10-277-233-220

; Sequence 220, Application US/10277233
; Publication No. US20030232750A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfile, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTI-BIOTICS
; FILE REFERENCE: 660081.406C1
; CURRENT APPLICATION NUMBER: US/10/277,233
; CURRENT FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Limulus polyphemus
US-10-277-233-220

Query Match 87.6%; Score 106; DB 15; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.2e-06;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRMCRKCYKGYCYRKR 18
|||:|||||:
Db 1 RRMCRVCYKGFYRKR 18

RESULT 6
US-10-838-289-744
; Sequence 744, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Geo. Jimming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; TITLE OF INVENTION: NANOSHELLS
; FILE REFERENCE: CWRU-P01-040

CURRENT APPLICATION NUMBER: US/10/838,289
CURRENT FILING DATE: 2004-05-03
PRIOR APPLICATION NUMBER: US 60/502,429
PRIOR FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/467,389
PRIOR FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 756
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 744
LENGTH: 18
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Tumor targeting peptide
US-10-838-289-744

Query Match 87.6%; Score 106; DB 17; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.2e-06;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMCRKCYKGYCRKCR 18
|||:|:|:|:|:|:|
DB 1 RRMCFRCYCRGFCYRKR 18

RESULT 7

US-09-030-619-219
Sequence 219, Application US/09030619B
Patent No. US20020035061A1
GENERAL INFORMATION:
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfile, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 219
LENGTH: 18
TYPE: PRT
ORGANISM: Limulus polyphemus
US-09-030-619-219

Query Match 85.1%; Score 103; DB 9; Length 18;
Best Local Similarity 77.8%; Pred. No. 2.9e-06;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMCRKCYKGYCRKCR 18
|||:|:|:|:|:|:|
DB 1 RRMCFRCYCRGFCYRKR 18

RESULT 8

US-09-912-609-107
Sequence 107, Application US/09912609
Publication No. US20020041898A1
GENERAL INFORMATION:
APPLICANT: UNGER, EVAN C.
APPLICANT: MATSUNAGA, TERRY ONICHI
APPLICANT: RAMASWAMI, VARADARAJAN
APPLICANT: ROMANOWSKI, MAREK J.
TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
FILE REFERENCE: 5030-0001.24
CURRENT APPLICATION NUMBER: US/09/912,609
CURRENT FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 09/703,474

PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: 09/478,124
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 107
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-912-609-107

Query Match 85.1%; Score 103; DB 9; Length 18;
Best Local Similarity 77.8%; Pred. No. 2.9e-06;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMCRKCYKGYCRKCR 18
|||:|:~|:|:|:|:|
DB 1 RRMCFRCYCRGFCYRKR 18

RESULT 9

US-10-042-872-13
Sequence 13, Application US/10042872
Publication No. US20020156017A1
GENERAL INFORMATION:
APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
APPLICANT: Hancock, Robert E. W.
APPLICANT: Zhang, Lijuan
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND METHODS OF
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: UBC1170-1
CURRENT APPLICATION NUMBER: US/10/042,872
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 09/604,864
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 18
TYPE: PRT
ORGANISM: Limulus polyphemus
US-10-042-872-13

Query Match 85.1%; Score 103; DB 13; Length 18;
Best Local Similarity 77.8%; Pred. No. 2.9e-06;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMCRKCYKGYCRKCR 18
|||:|:~|:|:|:|:|
DB 1 RRMCFRCYCRGFCYRKR 18

RESULT 10

US-10-277-232-219
Sequence 219, Application US/10277232
Publication No. US20030211537A1
GENERAL INFORMATION:
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfile, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406C1
CURRENT APPLICATION NUMBER: US/10/277,232
CURRENT FILING DATE: 2002-11-27
NUMBER OF SEQ ID NOS: 232

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 219
LENGTH: 18
TYPE: PRT
ORGANISM: Limulus polyphemus
US-10-277-232-219

Query Match 85.1%; Score 103; DB 15; Length 18;
Best Local Similarity 77.8%; Pred. No. 2.9e-06;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMCRYKCYKGYCKR 18
|||:|:|:|:|:|:|
DB 1 RRMCFRCVCRGFCYKCR 18

RESULT 11
US-10-277-233-219
Sequence 219, Application US/102772233
Publication No. US20030232750A1

GENERAL INFORMATION:
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Britle, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H. P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
FILE REFERENCE: 660081.406C1
CURRENT FILING DATE: US/10/277,233
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 219
LENGTH: 18
TYPE: PRT
ORGANISM: Limulus polyphemus
US-10-277-233-219

Query Match 85.1%; Score 103; DB 15; Length 18;
Best Local Similarity 77.8%; Pred. No. 2.9e-06;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMCRYKCYKGYCKR 18
|||:|:|:|:|:|:|
DB 1 RRMCFRCVCRGFCYKCR 18

RESULT 12
US-10-838-289-743
Sequence 743, Application US/10838289
Publication No. US20050058603A1

GENERAL INFORMATION:
APPLICANT: Gao, Jiming
APPLICANT: Ai, Hua
TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
TITLE OF INVENTION: NANOSHELLS
FILE REFERENCE: CWRU-P01-040
CURRENT APPLICATION NUMBER: US/10/838,289
CURRENT FILING DATE: 2004-05-03
PRIOR APPLICATION NUMBER: US 60/502,429
PRIOR FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/467,389
PRIOR FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 756
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 743
LENGTH: 18
TYPE: PRT
ORGANISM: Unknown
FEATURE:

OTHER INFORMATION: Tumor targeting peptide
US-10-838-289-743

Query Match 85.1%; Score 103; DB 17; Length 18;
Best Local Similarity 77.8%; Pred. No. 2.9e-06;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMCRYKCYKGYCKR 18
|||:|:|:|:|:|:|
DB 1 RRMCFRCVCRGFCYKCR 18

RESULT 13
US-10-042-872-18
Sequence 18, Application US/10042872
Publication No. US20020156017A1

GENERAL INFORMATION:
APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
APPLICANT: Hancock, Robert E. W.
APPLICANT: Zhang, Lijuan
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND METHODS OF
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: UBC1170-1
CURRENT APPLICATION NUMBER: US/10/042,872
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 09/604,864
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: cationic antimicrobial peptide
NAME/KEY: VARIANT
LOCATION: 5
OTHER INFORMATION: Xaa is an amino acid having a basic side chain
FEATURE:
NAME/KEY: VARIANT
LOCATION: 10
OTHER INFORMATION: Xaa is an amino acid having an aromatic side chain or an aliphatic
US-10-042-872-18

Query Match 79.3%; Score 96; DB 13; Length 18;
Best Local Similarity 77.8%; Pred. No. 2.1e-05;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRMCRYKCYKGYCKR 18
|||:|:|:|:|:|:|
DB 1 RRMCFRCVCRGFCYKCR 18

RESULT 14
US-10-042-872-10
Sequence 10, Application US/10042872
Publication No. US20020156017A1

GENERAL INFORMATION:
APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
APPLICANT: Hancock, Robert E. W.
APPLICANT: Zhang, Lijuan
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND METHODS OF
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: UBC1170-1
CURRENT APPLICATION NUMBER: US/10/042,872
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 09/604,864
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 18

TYPE: PRT
ORGANISM: Limulus polyphemus
US-10-042-872-10

Query Match 78.5%; Score 95; DB 13; Length 18;
Best Local Similarity 77.8%; Pred. No. 2.9e-05;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RMCYRKCYKGYCRKCR 18
||| | | | | | | | | | | | | | | | | | | |
DB 1 RMCRCVVCYAGFCYRKCR 18

RESULT 15

US-09-030-619-229
Sequence 229, Application US/09030619B
Patent No. US20020035061A1
GENERAL INFORMATION:
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfile, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: McNicol, Patricia J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
FILE REFERENCE: 660081.406
CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 229
LENGTH: 17
TYPE: PRT
ORGANISM: Tachypleus tridentatus
US-09-030-619-229

Query Match 77.7%; Score 94; DB 9; Length 17;
Best Local Similarity 76.5%; Pred. No. 3.6e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 RMCYRKCYKGYCRKCR 18
||| | | | | | | | | | | | | | | | | | | |
DB 1 RMCRCVVCYAGFCYRKCR 17

Search completed: May 9, 2005, 21:18:18
Job time : 134 secs

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